```
<!--StartFragment-->RESULT 1
Q9ZRC7_ALNGL
ID   Q9ZRC7_ALNGL            Unreviewed;        99 AA.
AC   Q9ZRC7;
DT   01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1999, sequence version 1.
DT   24-JUL-2007, entry version 22.
DE   Actinorizal nodulin AgNOD-GHRP.
GN   Name=agNt84;
OS   Alnus glutinosa (Alder).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   rosids; eurosids I; Fagales; Betulaceae; Alnus.
OX   NCBI_TaxID=3517;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Root nodules;
RA   Dobritsa S.V., Mullin B.C.;
RT   "In vitro expression of actinorhizal nodulin AgNOD-GHRP and
RT   demonstration of its toxicity ot Escherichia coli.";
RL   (In) Stacey G., Mullin B.C., Gresshoff P.M. (eds.);
RL   THE BIOLOGY OF PLANT-MICROBE INTERACTIONS: PROCEEDINGS OF THE 8TH
RL   INTERNATIONAL SYMPOSIUM ON MOLECULAR PLANT-MICROBE INTERACTIONS,
RL   pp.1-1, Unknown Publisher (1996).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Root nodules;
RA   Twigg P.G.;
RT   "Isolation of a nodule-specific cDNA encoding a putative glycine-rich
RT   protein from Alnus glutinosa.";
RL   Thesis (1993), The University of Tennessee, Knoxville, TN, USA.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Root nodules;
RA   Pawlowski K., Twigg P.G., Dobritsa S.V., Guan C., Mullin B.C.;
RT   "A nodule-specific gene family from Alnus glutinosa encodes glycine
RT   and histidine-rich proteins expressed in the early stages of
RT   actinorhizal nodule development.";
RL   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U69156; AAD00171.1; -; mRNA.
DR   InterPro; IPR010800; GRP.
DR   Pfam; PF07172; GRP; 1.
PE   4: Predicted;
SQ   SEQUENCE   99 AA;  10567 MW;  2ACBE4D57C070E83 CRC64;

  Query Match             100.0%;  Score 34;  DB 2;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-28;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HGHRHVHGHGHGHVHGNGNEHGHGHHHGRGHPGH 34
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Db         50 HGHRHVHGHGHGHVHGNGNEHGHGHHHGRGHPGH 83
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